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Cant  
using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

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**IN THE CLAIMS:**

Please cancel claims 32, 39, and 42 without prejudice to or disclaimer of the subject matter recited therein.

Please amend claims 26, 30, 31, 34, 36, and 40 as follows (a marked-up version showing changes made is attached hereto):

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26. (amended) An isolated polynucleotide comprising a) a nucleotide sequence encoding a gamma tocopherol methyltransferase having a sequence identity of at least 80%, based on the Clustal method of alignment, when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8 and 28; or b) the complement of the nucleotide sequence wherein the complement and the nucleotide sequence have the same number of nucleotides and are 100% complementary.

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30. (amended) The polynucleotide of Claim 26 wherein the polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NOs:8 and 28.

31. (amended) The polynucleotide of Claim 26, wherein the polynucleotide comprises the nucleotide sequence selected from SEQ ID NOs:7 and 27.

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34. (amended) A transgenic cell or a virus comprising the polynucleotide of Claim 40.

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36. (amended) A transgenic plant comprising the polynucleotide of Claim 40.

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40. (amended) A chimeric gene comprising the polynucleotide of Claim 26 operably linked to at least one regulatory sequence.

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